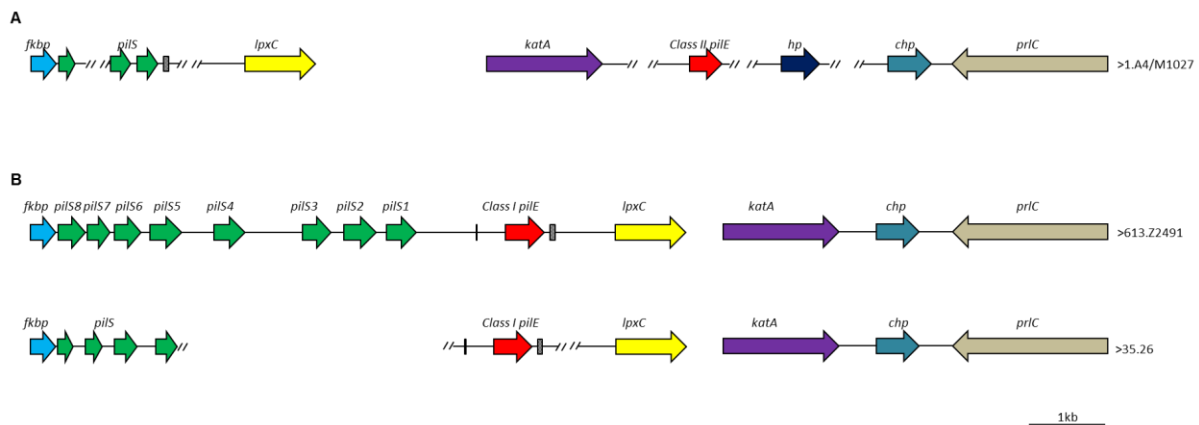


Additional file 10. Schematic diagrams of class II (A) and class I (B) *pilE* genes in genomes from meningococcal isolates belonging to clonal complex 4.



Identification code and name (>ID.name) of each isolate are indicated. Due to the draft nature of the genomes of isolates A4/M1027 and 26, it is not possible to ascertain the genomic context of the *pilE* gene and the assembly depicted is based upon the arrangement of genes in typical class I or class II loci, with the end of each contig indicated by diagonal lines. The presence of the *hp* gene in isolate A4/M1027 is consistent with all genomes harbouring a class II *pilE* allele, as is the absence of any obvious guanine quartet (G4) sequence in the region 5' to the *pilE* coding sequence. In contrast, both the G4 and *Sma*/*Cla* sequences are detected adjacent to *pilE* in isolate 26, and there is no class II *pilE* or *hp* gene in the *katA* region. Thus, we conclude that within clonal complex 4, strains can have either a class I or a class II *pilE* arrangement.

Putative G4 sequences are shown as black lines and *Sma*/*Cla* sequences are shown as hatched boxes. *lpxC*: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase), *fkbp*: peptidyl-prolyl cis-trans isomerase, *pilS* : silent *pilS* cassettes, *pilE*: gene encoding major pilin

subunit, *katA*: catalase, *hp*: hypothetical protein, *chp*: conserved hypothetical protein, *prlC*: putative oligopeptidase Scale bar represents 1kb.